


Exhibit 3

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P41773

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Entry information

Entry name	LIPB_PSEFL
Primary accession number	P41773
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 32, November 1995
Sequence was last modified in	Release 32, November 1995
Annotations were last modified in	Release 46, February 2005
Name and origin of the protein	
Protein name	Lipase [Precursor]
Synonyms	EC 3.1.1.3 Triacylglycerol lipase
Gene name	None
From	<i>Pseudomonas fluorescens</i> [TaxID: 294]
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.

References

[1] NUCLEOTIDE SEQUENCE.

STRAIN=B52;

MEDLINE=92286777;PubMed=1599260 [NCBI, ExPASy, EBI, Israel, Japan]

Tan Y., Miller K.J.;

"Cloning, expression, and nucleotide sequence of a lipase gene from *Pseudomonas fluorescens* B52.";

Appl. Environ. Microbiol. 58:1402-1407(1992).

Comments

- **CATALYTIC ACTIVITY:** Triacylglycerol + H₂O = diacylglycerol + a carboxylate.
- **SIMILARITY:** Belongs to the AB hydrolase superfamily. Lipase family.

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Cross-references

EMBL M86350; AAA25882.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]

PIR A43942; A43942.
IPR001343; Hemlysn_Ca_bind.
IPR002921; Lipase_3.
InterPro IPR008262; Lipase_AS.
IPR000379; Ser_estrs.
IPR011049; Serralysn_like_C.
Graphical view of domain structure.
PF00353; HemolysinCabind; 3.
Pfam PF01764; Lipase_3; 1.
Pfam graphical view of domain structure.
PRINTS PR00313; CABNDNGRPT.
PROSITE PS00330; HEMOLYSIN_CALCIUM; 1.
PS00120; LIPASE_SER; 1.
ProDom [Domain structure / List of seq. sharing at least 1 domain]
HOBACGEN [Family / Alignment / Tree]
BLOCKS P41773.
ProtoNet P41773.
ProtoMap P41773.
PRESAGE P41773.
DIP P41773.
ModBase P41773.
SMR P41773; FC38C080F0A3BC55.
SWISS-2DPAGE Get region on 2D PAGE.
UniRef View cluster of proteins with at least 50% / 90% identity.

Keywords

Hydrolase; Lipid degradation; Signal.

Features



Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	23	23	Potential.
CHAIN	24	476	453	Lipase.
ACT_SITE	207	207		Charge relay system (by similarity).

Sequence information

Length: 476 AA [This is the length of the unprocessed precursor] Molecular weight: 50239 Da [This is the MW of the unprocessed precursor] CRC64: FC38C080F0A3BC55 [This is a checksum on the sequence]

```

10      20      30      40      50      60
MGIFDYKNLG TEGSKTLFAD AMAITLYSYH NLDNGFAVGY QHNLGLGLP ATLVGALLGS

70      80      90     100     110     120
TDSQGVIPGI PWNPDSEKAA LEAVQKAGWT PISASALGYA GKVDARGTFF GEKAGYTAAQ

130     140     150     160     170     180
VEVLGKYDDA GKLLIEIGIGF RGTSGPRETL ISDSIGDLIS DLLAALGPKD YAKNYAGEAF
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190      200      210      220      230      240
GGLLNVDY AGAHGLTGKD VVVSCHSLGG LAVNSMADLS NYKWAGFYKD ANYVAYASPT

250      260      270      280      290      300
QSAGDKVLNI GYENDPVFRA LDGSSFNLS LGVHDKPHES TTDNIVSFND HYASTLWNVL

310      320      330      340      350      360
PFSIVNLPTW VSHLPTAYGD GMTRILESGF YDQMTDSTV IVANLSDPAR ANTWWQDLNR

370      380      390      400      410      420
NAEPHKGNTF IIGSDGNOLI QGGNGADFIE GKGNDTIRD NSGHNTFLFS GHFGNDRVIG

430      440      450      460      470
YQPTDKLVFK DVQGSTDLRD HAKVVGADTV LTFGADSVTL VGVGHGGLWT EGVVIG

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P41773 in FASTA
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BLAST BLAST submission on
ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)



ScanProsite, MotifScan



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